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ANSWER 5 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4

AN 1979:571063 CAPLUS
DN 91:171063
ED Entered STN: 12 May 1984
TI Two-dimensional gel electrophoresis and computer analysis of proteins synthesized by clonal cell lines
AU Garrels, James I.
CS Neurobiol. Lab., Salk Inst., San Diego, CA, 92112, USA
SO Journal of Biological Chemistry (1979), 254(16), 7961-77
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
CC 9-3 (Biochemical Methods)
AB An improved method of 2-dimensional gel electrophoresis was developed which produced high resolution, reproducible images suitable for computer anal. In the images that were presented, >800 proteins were resolved without significant overlap, and many more proteins can be detected after longer exposures. To establish the usefulness of such methods for detailed quant. comparisons of cultured cells, extensive controls were carried out to test the reproducibility of the electrophoretic procedures, the same preparation procedures, and the cell culture conditions. A computerized scanning system was developed which can automatically detect and integrate the densities of the spots on a 2-dimensional fluorogram or autoradiogram. The corresponding proteins from 2 samples can then be matched and their intensities compared. Several types of graphic output have been used to display the number and magnitude of the differences between the compared samples. These methods were used to study the patterns of protein synthesis in the nerve cell lines B103 and the glial cell line B9. Both exponentially dividing and stationary cultures were analyzed and the relative rates of synthesis of .apprx.300 proteins were compared by computer. For each cell line, no major qual. differences were found between dividing and stationary phase cells although numerous quant. differences of up to 15-fold were detected. When the 2 cell lines were analyzed in the same state of growth and compared by computer, qual. differences were found in .apprx.5% of the proteins analyzed, and ≥40% of the shared proteins were involved in quant. differences of ≥2-fold. The rates of synthesis of the shared proteins were more divergent between the 2 cell lines than between dividing and stationary phase cells of either line. Thus, these cell lines can be therefore be distinguished, regardless of growth state, by their cell-specific proteins and by their characteristic rates of synthesis of many of the shared proteins.
ST protein electrophoresis nerve cell; glial cell protein electrophoresis
IT Proteins
RL: ANST (Analytical study)
(electrophoresis of, of glial and nerve cell, computer application in)
IT Computer application
(in protein electrophoresis of glial and nerve cells)
IT Nerve, composition
Neuroglia
(protein electrophoresis of cells of, computer application in)
IT Electrophoresis and Ionophoresis
(gel, of proteins, on polyacrylamide, computer application in)

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ST protein electrophoresis nerve cell; glial cell protein electrophoresis
IT Proteins
RL: ANST (Analytical study)
(electrophoresis of, of glial and nerve cell, computer application in)
IT Computer application
(in protein electrophoresis of glial and nerve cells)
IT Nerve, composition
Neuroglia
(protein electrophoresis of cells of, computer application in)
IT Electrophoresis and Ionophoresis
(gel, of proteins, on polyacrylamide, computer application in)

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ANSWER 6 OF 8 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
DUPLICATE 4
AN 1991:45325 BIOSIS
DN PREV199191023606; BA91:23606
TI UV IMAGING DENSITOMETRY OF UNSTAINED GELS FOR TWO-DIMENSIONAL ELECTROPHORESIS.
AU YAMAMOTO H [Reprint author]; NAKATANI M; SHINYA K; KIM B-H; KAKUNO T
CS SHIMADZU CORP, NAKAGYO-KU, KYOTO 604, JPN
SO Analytical Biochemistry, (1990) Vol. 191, No. 1, pp. 58-64.
CODEN: ANBCA2. ISSN: 0003-2697.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 10 Jan 1991
Last Updated on STN: 10 Jan 1991
AB A system suitable for ultraviolet imaging densitometry of two-dimensional electrophoretic gels that are unstained is described, together with its applications. A flying-spot densitometer linked with a personal computer was used for data acquistion, generation of mapping data, and image processing. Randomly distributed zones of proteins on two-dimensional gels were detected at 280 nm without being stained by two-dimensional scanning, and the densitometric value of each pixel (0.2 + 0.2 mm) was memorized by the computer, which generated a mapping pattern with density contours. The amount and densitometric value of cytochrome c had a linear relationship in the range of 2-200 μg. Zone locations of bovine linear proteins separated on two-dimensional gels were indicated on a map expressed in X-Y coordinates, and the pIs and molecular weights could be calculated from the map by use of pI and molecular weight markers on the same gel.
CC General biology - Information, documentation, retrieval and computer applications 00530
Biochemistry methods - Proteins, peptides and amino acids 10054
Biochemistry studies - Proteins, peptides and amino acids 10064
Biophysics - Methods and techniques 10504
IT Major Concepts
Biochemistry and Molecular Biophysics; Computer Applications (Computational Biology); Methods and Techniques
IT Miscellaneous Descriptors
PROTEINS COMPUTER ANALYSIS

ANSWER 7 OF 7 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4

AN 1982:16881 CAPLUS

DN 96:16881

ED Entered STN: 12 May 1984

TI The TYCHO system for computer analysis of two-dimensional gel electrophoresis patterns

AU Anderson, N. L.; Taylor, J.; Scandora, A. E.; Coulter, B. P.; Anderson, N. G.

CS Div. Biol. Med. Res., Argonne Natl. Lab., Argonne, IL, 60439, USA

SO Clinical Chemistry (Washington, DC, United States) (1981), 27(11), 1807-20
CODEN: CLCHAU; ISSN: 0009-9147

DT Journal

LA English

CC 9-7 (Biochemical Methods)

AB A computer system for the anal. of high-resolution 2-dimensional gel-electrophoresis patterns, and some initial applications are described. The system (called TYCHO) comprises programs for image acquisition, background subtraction and smoothing, spot detection, gaussian spot modeling, and pattern matching and comparison. It is based on a conventional minicomputer, but makes extensive use of a high-speed array processor in the image-processing and -modeling steps. Used in concert with the ISO-DALT 2-dimensional electrophoresis system (Anderson, N. G.; Anderson, N. L., 1978), TYCHO allows quant. measurement of hundreds of proteins in complex biol. samples, and constitutes the initial data-reduction system required for work towards a Human Protein Index.

ST protein electrophoresis computer analysis

IT Proteins
RL: ANST (Analytical study)
(electrophoresis of, computer anal. of)

IT Electrophoresis and Ionophoresis
(of proteins, computer anal. of)

IT Computer application
(to electrophoresis of proteins)

ANSWER 6 OF 7 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
AN 1982:213710 CAPLUS
DN 96:213710
ED Entered STN: 12 May 1984
TI Some relatively simple steps toward a computer system for the analysis of two-dimensional gel -electrophoresis autoradiographs
AU Fox, Stanley H.
CS Med. Cent., Univ. Cincinnati, Cincinnati, OH, 45267, USA
SO Clinical Chemistry (Washington, DC, United States) (1982), 28(4, Pt. 2), 932-4
CODEN: CLCHAU; ISSN: 0009-9147
DT Journal
LA English
CC 9-7 (Biochemical Methods)
Section cross-reference(s): 80
AB A computerized system for the quant. comparison of 2-dimensional polyacrylamide gel autoradiographs is being developed that requires relatively limited hardware resources. Two fast, simple, and stable programs, one for background and streak subtraction and one for peak detection, were developed and tested. Two methods developed by others, one for image smoothing and one for peak matching, also were tested. A very simple spot-d. integration program that works on isolated spots has been written and is being developed further.
ST polyacrylamide gel autoradiog computer analysis; electrophoresis autoradiog computer analysis; protein electrophoresis autoradiog computer
IT Proteins
RL: ANT (Analyte); ANST (Analytical study)
(determination of, by 2-dimensional gel electrophoresis and autoradiog., computerized anal. of)
IT Computer application
(in proteins determination by 2-dimensional gel electrophoresis and autoradiog.)
IT Radiography
(auto-, of proteins, after 2-dimensional gel electrophoresis, computerized anal. of)
IT Electrophoresis and Ionophoresis
(gel, two-dimensional, of proteins, autoradiog. combined with, computerized anal. of)

ANSWER 6 OF 7 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
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ST polyacrylamide gel autoradiog computer analysis; electrophoresis autoradiog computer analysis; protein electrophoresis autoradiog computer
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RL: ANT (Analyte); ANST (Analytical study)
(determination of, by 2-dimensional gel electrophoresis and autoradiog., computerized anal. of)
IT Computer application
(in proteins determination by 2-dimensional gel electrophoresis and autoradiog.)
IT Radiography
(auto-, of proteins, after 2-dimensional gel electrophoresis, computerized anal. of)
IT Electrophoresis and Ionophoresis
(gel, two-dimensional, of proteins, autoradiog. combined with, computerized anal. of)

ANSWER 4 OF 5 JAPIO (C) 2006 JPO on STN
AN 1986-129562 JAPIO
TI QUANTITATIVE COMPARISON DEVICE FOR MIGRATION IMAGE
IN NISHINE TSUTOMU
PA SHIMADZU CORP
PI JP 61129562 A 19860617 Showa
AI JP 1984-251401 (JP59251401 Showa) 19841128
PRAI JP 1984-251401 19841128
SO PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined Applications, Vol. 1986
IC ICM G01N027-26
ICS G01N021-17
AB PURPOSE: To measure quantitatively protein components with high accuracy by using the migration spot of a protein component having a known migration pattern as a reference, comparing the protein component having an unknown migration pattern in a vital sample with the reference.
CONSTITUTION: A two-dimensional migration gel 4 in which the protein components are migrated is divided to, for example, 4 regions 10a, 10b, 10c, 10d by isoelectric points. The standard material having the known migration pattern and mol.weight, for example, albumin, globulin or the like is preliminarily introduced into the gel 4. The standard material is measured, then the sample is measured in the optical concentration measurement. The variance in the dissipation quantity of the protein component dissipated from the two-dimensional gel by the gel equilibriating operation and gel dyeing operation after the end of the two-dimensional electrophoresis is thereby corrected and the quantitative comparison of the protein component in the same quantity of the sample migrated in the different two-dimensional gel is made possible.

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DUPLICATE 3
AN 1990:371554 BIOSIS
DN PREV199090058235; BA90:58235
TI A REVIEW OF THE CLIP SYSTEM FOR THE QUANTITATIVE ANALYSIS OF TWO-DIMENSIONAL ELECTROPHORESIS GELS.
AU POTTER D J [Reprint author]
CS DEP ELECTRICAL COMPUTER ENG, CLARKSON UNIV, POTSDAM, NY 13676, USA
SO Electrophoresis, (1990) Vol. 11, No. 5, pp. 415-419.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 21 Aug 1990
Last Updated on STN: 21 Aug 1990
AB This paper reviews th CLIP image processing system for the complete analysis of two-dimensional electrophoresis images. The analysis problem for two-dimensional gel images can be broken down into three issues: segmentation of individual gel images, alignment and comparison of pairs of gel images, and information storage and retrieval. This paper describes these problems and reviews how the CLIP system handles each of them. Segmentation is the location and isolation of each protein spot on an individual gel image and also the extraction of individual spot data such as position, area and volume. There are three basic stages; background field correction, noise filtering, spot detection and information extraction. Alignment and comparison of gel images involves matching protein spots between two gels. This can be quite difficult because there is not a simple relationship which can transform one gel image onto another. The database issues concern storing all the information which has been obtained from the above operations such that retrieval of this information can be readily performed. The advantage of the CLIP system over others is speed of processing. CLIP series computers use one processor for every pixel of the camera image such that image processing algorithms run in parallel. The main disadvantage is in the cost of these machines. With the declining trend in the cost of parallel processors, these machines will become more and more viable alternatives. This paper reviews the algorithms for the analysis of two-dimensional gels. It is shown that CLIP is flexible enough to perform more than one type of algorithm for a particular operation.
CC General biology - Information, documentation, retrieval and computer applications 00530
Mathematical biology and statistical methods 04500
Biochemistry methods - Proteins, peptides and amino acids 10054
Biochemistry studies - Proteins, peptides and amino acids 10064
Biophysics - Methods and techniques 10504
Biophysics - Molecular properties and macromolecules 10506
IT Major Concepts
Biochemistry and Molecular Biophysics; Computer Applications (Computational Biology); Mathematical Biology (Computational Biology); Methods and Techniques
IT Miscellaneous Descriptors
PROTEIN ANALYSIS COMPUTER APPLICATIONS

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LA ENGLISH
ED Entered STN: 21 Aug 1990
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Biochemistry studies - Proteins, peptides and amino acids 10064
Biophysics - Methods and techniques 10504
Biophysics - Molecular properties and macromolecules 10506
IT Major Concepts
Biochemistry and Molecular Biophysics; Computer Applications (Computational Biology); Mathematical Biology (Computational Biology); Methods and Techniques
IT Miscellaneous Descriptors
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